

SEQUENCE LISTING

Nohyaku Co., Ltd. <120> NOVEL PROTOPORPHYRINOGEN OXIDASE TOLERANT TO PHOTOBLEACING HERBICIDE <130> Q58140 <140> 09/508,418 <141> 2000-03-13 <150> JP 9-265084 <151> 1997-09-11 <160> 11 <170> PatentIn version 3.0 <210> 1 <211> 1874 <212> DNA <213> Nicotiana tabacum <220> <221> exon <222> (26)..(1672) <220> <221> misc_feature <223> Strain name: Xanthi NC <400> 1 agegeggtet acaagteagg eagte atg aca act eee ate gee aat eat 52 Met Thr Thr Pro Ile Ala Asn His cct aat att ttc act cac cag tcg tcg tca tcg cca ttg gca ttc tta 100 Pro Asn Ile Phe Thr His Gln Ser Ser Ser Pro Leu Ala Phe Leu 15 aac cgt acg agt ttc atc cct ttc tct tca atc tcc aag cgc aat agt 148 Asn Arg Thr Ser Phe Ile Pro Phe Ser Ser Ile Ser Lys Arg Asn Ser gtc aat tgc aat ggc tgg aga aca cga tgc tcc gtt gcc aaa gat tac 196 Val Asn Cys Asn Gly Trp Arg Thr Arg Cys Ser Val Ala Lys Asp Tyr 45 50 aca gtt cct tcc tca gcg gtc gac ggc gga ccc gcc gcg gag ctg gac 244 Thr Val Pro Ser Ser Ala Val Asp Gly Gly Pro Ala Ala Glu Leu Asp 60 65 tgt gtt ata gtt gga gca gga att agt ggc ctc tgc att gcg cag gtg 292 Cys Val Ile Val Gly Ala Gly Ile Ser Gly Leu Cys Ile Ala Gln Val

atç Met 90	g tco Ser	gct Ala	aat Asn	tac Tyr	e ccc Pro 95	aat Asn	ttg Leu	g atg Met	g gta : Val	acc Thr	Gli	g gcg ı Ala	g aga Arc	ı gat ı Asp	cgt Arg 105		340
gco Ala	ggt Gly	ggc Gly	aac Asn	ata Ile 110	. Thr	act Thr	gtg Val	gaa Glu	aga Arg 115	Asp	ggo Gly	tat Tyr	ttg Lev	tgg Trp 120	gaa Glu		388
gaa Glu	ggt Gly	ccc Pro	aac Asn 125	Ser	ttc Phe	cag Gln	ccg Pro	ser 130	Asp	cct Pro	ato Met	ttg Leu	act Thr 135	Met	gca Ala		436
gta Val	gat Asp	tgt Cys 140	Gly	ttg Leu	aag Lys	gat Asp	gat Asp 145	ttg Leu	gtg Val	ttg Leu	gga Gly	gat Asp 150	Pro	aat Asn	gcg Ala		484
ccc Pro	cgt Arg 155	Phe	gtt Val	ttg Leu	tgg Trp	aag Lys 160	ggt Gly	aaa Lys	tta Leu	agg Arg	ccc Pro 165	Val	ccc Pro	tca Ser	aaa Lys		532
ctc Leu 170	act Thr	gat Asp	ctt Leu	ccc Pro	ttt Phe 175	ttt Phe	gat Asp	ttg Leu	atg Met	agc Ser 180	att Ile	cct Pro	ggc	aag Lys	ttg Leu 185		580
aga Arg	gct Ala	ggt Gly	ttt Phe	ggt Gly 190	ccc Pro	att Ile	ggc Gly	ctc Leu	cgc Arg 195	cct Pro	tca Ser	cct Pro	cca Pro	ggt Gly 200	cat His		628
gag Glu	gaa Glu	tca Ser	gtt Val 205	gag Glu	cag Gln	ttc Phe	gtg Val	cgt Arg 210	cgt Arg	aat Asn	ctt Leu	ggt Gly	ggc Gly 215	gaa Glu	gtc Val		676
ttt Phe	gaa Glu	cgc Arg 220	ttg Leu	ata Ile	gaa Glu	cca Pro	ttt Phe 225	tgt Cys	tct Ser	ggt Gly	gtt Val	tat Tyr 230	gct Ala	ggt Gly	gat Asp		724
ccc Pro	tca Ser 235	aaa Lys	ctg Leu	agt Ser	atg Met	aaa Lys 240	gca Ala	gca Ala	ttt Phe	gly ggg	aaa Lys 245	gtt Val	tgg Trp	aag Lys	ttg Leu		772
gaa Glu 250	gaa Glu	act Thr	ggt Gly	ggt Gly	agc Ser 255	att Ile	att Ile	gga Gly	gga Gly	acc Thr 260	ttt Phe	aaa Lys	gca Ala	ata Ile	aag Lys 265	;	820
gag Glu	aga Arg	tcc Ser	agt Ser	aca Thr 270	cct Pro	aaa Lys	gcg Ala	ccc Pro	cgc Arg 275	gat Asp	ccg Pro	cgt Arg	tta Leu	cct Pro 280	aaa Lys		868
Pro	Lys	Gly	Gln 285	Thr	Val	gga Gly	Ser	Phe 290	Arg	Lys	Gly	Leu	Arg 295	Met	Leu	<u> </u>	916
ccg	gat	gca	atc	agt	gca	aga	ttg	gga	agc	aaa	tta	aaa	cta	tca	tgg	2	964

Pro	Asp	300		: Ser	Ala	. Arg	Leu 305		Ser	Lys	Leu	Lys 310		Ser	Trp	
		Ser										Tyr			aca Thr	1012
	Glu					Val					Ser				gtc Val 345	1066
					Tyr					Ile					tcg Ser	1108
															gga Gly	1156
gca Ala	gtc Val	aca Thr 380	Ile	tca Ser	tat Tyr	cct Pro	caa Gln 385	gaa Glu	gct Ala	att Ile	cgt Arg	gat Asp 390	gag Glu	cgt Arg	ctg Leu	1204
gtt Val	gat Asp 395	ggt Gly	gaa Glu	cta Leu	aag Lys	gga Gly 400	ttt Phe	ggg Gly	cag Gln	ttg Leu	cat His 405	cca Pro	cgt Arg	aca Thr	cag Gln	1252
gga Gly 410	gtg Val	gaa Glu	aca Thr	cta Leu	gga Gly 415	acg Thr	ata Ile	tat Tyr	agt Ser	tca Ser 420	tca Ser	ctc Leu	ttc Phe	cct Pro	aac Asn 425	1300
					cgg Arg											1348
aaa Lys	aat Asn	cct Pro	gaa Glu 445	att Ile	ttg Leu	tct Ser	aag Lys	acg Thr 450	gag Glu	agc Ser	caa Gln	ctt Leu	gtg Val 455	gaa Glu	gta Val	1396
					aga Arg											1444
cct Pro	ctt Leu 475	gtt Val	gtg Val	ggt Gly	gtg Val	cga Arg 480	gta Val	tgg Trp	cca Pro	caa Gln	gct Ala 485	atc Ile	cca Pro	cag Gln	ttt Phe	1492
					gat Asp 495											1540
					gly ggg											1588

gta gca ttg ggg agg tgt gtt gaa ggt gct tat gaa gtt gca tcc gag Val Ala Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Val Ala Ser Glu 525 530 535	1636
gta aca gga ttt ctg tct cgg tat gca tac aaa tga aacctgtgtt Val Thr Gly Phe Leu Ser Arg Tyr Ala Tyr Lys 540 545	1682
gggggtagtc caaaccttgt tagtagtacg atcatgcctt gggaaaattg gcatgtgcct	1742
aaaagttttg ctcattagag ttattttagc cttggtaaat gatttgtact tgatatcagt	1802
cgttttcttt gagataaaat gttcctgttc aggaaatata atgtatatca attttaaaca	1862
aaaaaaaaaa aa	1874
<210> 2 <211> 548 <212> PRT <213> Nicotiana tabacum <220> <221> misc_feature <223> Strain name: SR1	
<400> 2	
Met Thr Thr Pro Ile Ala Asn His Pro Asn Ile Phe Thr His Gln 1 5 10 15	
Ser Ser Ser Pro Leu Ala Phe Leu Asn Arg Thr Ser Phe Ile Pro 20 25 30	
Phe Ser Ser Ile Ser Lys Arg Asn Ser Val Asn Cys Asn Gly Trp Arg 35 40 45	
Thr Arg Cys Ser Val Ala Lys Asp Tyr Thr Val Pro Ser Ser Ala Val 50 55 60	
Asp Gly Gly Pro Ala Ala Glu Leu Asp Cys Val Ile Val Gly Ala Gly 65 70 75 80	
Ile Ser Gly Leu Cys Ile Ala Gln Val Met Ser Ala Asn Tyr Pro Asn 85 90 95	
Leu Met Val Thr Glu Ala Arg Asp Arg Ala Gly Gly Asn Ile Thr Thr 100 105 110	
Val Glu Arg Asp Gly Tyr Leu Trp Glu Glu Gly Pro Asn Ser Phe Gln 115 120 125	
Pro Ser Asp Pro Met Leu Thr Met Ala Val Asp Cys Gly Leu Lys Asp 130 135 140	

Asp 145	Leu	Val	Leu	Gly	Asp 150	Pro	Asn	Ala	Pro	Arg 155	Phe	Val	Leu	Trp	Lys 160
Gly	Lys	Leu	Arg	Pro 165	Val	Pro	Ser	Lys	Leu 170	Thr	Asp	Leu	Pro	Phe 175	Phe
Asp	Leu	Met	Ser 180	Ile	Pro	Gly	Lys	Leu 185	Arg	Ala	Gly	Phe	Gly 190	Pro	Ile
Gly	Leu	Arg 195	Pro	Ser	Pro	Pro	Gly 200	His	Glu	Glu	Ser	Val 205	Glu	Gln	Phe
Val	Arg 210	Arg	Asn	Leu	Gly	Gly 215	Glu	Val	Phe	Glu	Arg 220	Leu	Ile	Glu	Pro
Phe 225	Cys	Ser	Gly	Val	Tyr 230	Val	Gly	Asp	Pro	Ser 235	Lys	Leu	Ser	Met	Lys 240
Ala	Ala	Phe	Gly	Lys 245	Val	Trp	Lys	Leu	Glu 250	Glu	Thr	Gly	Gly	Ser 255	Ile
Ile	Gly	Gly	Thr 260	Phe	Lys	Ala	Ile	Lys 265	Glu	Arg	Ser	Ser	Thr 270	Pro	Lys
Ala	Pro	Arg 275	Asp	Pro	Arg	Leu	Pro 280	Lys	Pro	Lys	Gly	Gln 285	Thr	Val	Gly
Ser	Phe 290	Arg	Lys	Gly	Leu	Arg 295	Met	Leu	Pro	Asp	Ala 300	Ile	Ser	Ala	Arg
Leu 305	Gly	Ser	Lys	Leu	Lys 310	Leu	Ser	Trp	Lys	Leu 315	Ser	Ser	Ile	Thr	Lys 320
Ser	Glu	Lys	Gly	Gly 325	Tyr	His	Leu	Thr	Tyr 330	Glu	Thr	Pro	Glu	Gly 335	Val
Val	Ser	Leu	Gln 340	Ser	Arg	Ser	Ile	Val 345	Met	Thr	Val	Pro	Ser 350	Tyr	Val
Ala	Ser	Asn 355	Ile	Leu			Leu 360		Val	Ala		Ala 365	Asp	Ala	Leu
Ser	Asn 370	Phe	Tyr	Tyr	Pro	Pro 375	Val	Gly	Ala	Val	Thr 380	Ile	Ser	Tyr	Pro
Gln 385	Glu	Ala	Ile	Arg	Asp 390	Glu	Arg	Leu	Val	Asp 395	Gly	Glu	Leu	Lys	Gly 400
Phe	Gly	Gln	Leu	His 405	Pro	Arg	Thr	Gln	Gly 410	Val	Glu	Thr	Leu	Gly 415	Thr
Ile	Tyr	Ser	Ser	Ser	Leu	Phe	Pro	Asn 425	Arg	Ala	Pro	Lys	Gly 430	Arg	Val

Let	ı Let	1 Let 435	ı Asn	Tyr	Ile	Gly	Gly 440		Lys	Asn	Pro	Glu 445		Leu	Ser	
Lys	450	Glu	Ser	Gln	Leu	Val 455	Glu	Val	Val	Asp	Arg 460		Leu	Arg	Lys	
Met 465		Ile	. Lys	Pro	Lys 470	Ala	Gln	Asp	Pro	Leu 475		Val	Gly	Val	Arg 480	
Val	Trp	Pro	Gln	Ala 485	Ile	Pro	Gln	Phe	Leu 490		Gly	His	Leu	Asp 495	Thr	
Leu	Ser	Thr	Ala 500	Lys	Ala	Ala	Met	Asn 505	Asp	Asn	Gly	Leu	Glu 510	Gly	Leu	
Phe	Leu	Gly 515	Gly	Asn	Tyr	Val	Ser 520	Gly	Val	Ala	Leu	Gly 525		Cys	Val	
Glu	Gly 530	Ala	Tyr	Glu	Val	Ala 535	Ser	Glu	Val	Thr	Gly 540	Phe	Leu	Ser	Arg	
Tyr 545	Ala	Tyr	Lys													
<21 <21		3 1874														
<21	2 > 1	DNA	tiana	a tak	oacur	n										
<22								-								
<22 <22		exon (26)	(16	572)												
<22			feat													
			in na		SR1											
<40	0 > 3	3														
agc	geggt	ict a	acaag	tcag	g ca								gcc Ala			52
cct Pro	aat Asn	att Ile	ttc Phe	act Thr	cac His	cag Gln	tcg Ser	tcg Ser	tca Ser	tcg Ser	cca Pro	ttg Leu	gca Ala	ttc Phe	tta Leu	100
10					15					20					25	
			agt Ser					Ser								148
			aat Asn 45				Thr									196

aca Thr	gtt Val	cct Pro 60	tcc Ser	tca Ser	gcg Ala	gtc Val	gac Asp 65	ggc Gly	gga Gly	ccc Pro	gcc Ala	gcg Ala 70	gag Glu	ctg Leu	gac Asp	244
tgt Cys	gtt Val 75	ata Ile	gtt Val	gga Gly	gca Ala	gga Gly 80	att Ile	agt Ser	ggc Gly	ctc Leu	tgc Cys 85	att Ile	gcg Ala	cag Gln	gtg Val	292
	tcc Ser															340
gcc Ala	ggt Gly	ggc Gly	aac Asn	ata Ile 110	acg Thr	act Thr	gtg Val	gaa Glu	aga Arg 115	gac Asp	ggc Gly	tat Tyr	ttg Leu	tgg Trp 120	gaa Glu	388
gaa Glu	ggt Gly	ccc Pro	aac Asn 125	agt Ser	ttc Phe	cag Gln	ccg Pro	tcc Ser 130	gat Asp	cct Pro	atg Met	ttg Leu	act Thr 135	atg Met	gca Ala	436
gta Val	gat Asp	tgt Cys 140	gga Gly	ttg Leu	aag Lys	gat Asp	gat Asp 145	ttg Leu	gtg Val	ttg Leu	gga Gly	gat Asp 150	cct Pro	aat Asn	gcg Ala	484
ccc Pro	cgt Arg 155	ttc Phe	gtt Val	ttg Leu	tgg Trp	aag Lys 160	ggt Gly	aaa Lys	tta Leu	agg Arg	ccc Pro 165	gtc Val	ccc Pro	tca Ser	aaa Lys	532
ctc Leu 170	act Thr	gat Asp	ctt Leu	ccc Pro	ttt Phe 175	ttt Phe	gat Asp	ttg Leu	atg Met	agc Ser 180	att Ile	cct Pro	ggc Gly	aag Lys	ttg Leu 185	580
	gct Ala															628
gag Glu	gaa Glu	tca Ser	gtt Val 205	gag Glu	cag Gln	ttc Phe	gtg Val	cgt Arg 210	cgt Arg	aat Asn	ctt Leu	ggt Gly	ggc Gly 215	gaa Glu	gtc Val	676
ttt Phe	gaa Glu	cgc Arg 220	ttg Leu	ata Ile	gaa Glu	cca Pro	ttt Phe 225	tgt Cys	tct Ser	ggt Gly	gtt Val	tat Tyr 230	gtt Val	ggt Gly	gat Asp	724
ccc Pro	tca Ser 235	aaa Lys	ctg Leu	agt Ser	atg Met	aaa Lys 240	gca Ala	gca Ala	ttt Phe	gly ggg	aaa Lys 245	gtt Val	tgg Trp	aag Lys	ttg Leu	772
gaa Glu 250	gaa Glu	act Thr	ggt Gly	ggt Gly	agc Ser 255	att Ile	att Ile	gga Gly	gga Gly	acc Thr 260	ttt Phe	aaa Lys	gca Ala	ata Ile	aag Lys 265	820
	aga Arg															868

cca Pro	aaa Lys	gga	cag Gln 285	Thr	gtt Val	gga Gly	tca Ser	Phe 290	e Arg	, aac , Lys	ggt Gly	cto Let	aga Arg 295	, Met	g ctg : Leu	916
ccg Pro	gat Asp	gca Ala 300	Ile	agt Ser	gca Ala	aga Arg	ttg Leu 305	Gly	ago Ser	: aaa · Lys	tta Leu	aaa Lys 310	. Leu	tca Sei	tgg Trp	964
aag Lys	ctt Leu 315	tct Ser	agc Ser	att Ile	act Thr	aag Lys 320	tca Ser	gaa Glu	aaa Lys	gga Gly	gga Gly 325	Tyr	cac His	ttg Lev	aca Thr	1012
tac Tyr 330	gag Glu	aca Thr	cca Pro	gaa Glu	gga Gly 335	gta Val	gtt Val	tct Ser	ctt Leu	caa Gln 340	Ser	cga Arg	agc Ser	att	gtc Val 345	1060
atg Met	act Thr	gtg Val	cca Pro	tcc Ser 350	tat Tyr	gta Val	gca Ala	agc Ser	aac Asn 355	ata Ile	tta Leu	cgt Arg	cct Pro	ctt Leu 360	tcg Ser	1108
gtt Val	gcc Ala	gca Ala	gca Ala 365	gat Asp	gca Ala	ctt Leu	tca Ser	aat Asn 370	ttc Phe	tac Tyr	tat Tyr	ccc Pro	cca Pro 375	gtt Val	gga Gly	['] 1156
Ala	Val	Thr 380	Ile	Ser	Tyr	cct Pro	Gln 385	Glu	Ala	Ile	Arg	Asp 390	Glu	Arg	Leu	1204
gtt Val	gat Asp 395	ggt Gly	gaa Glu	cta Leu	aag Lys	gga Gly 400	ttt Phe	ggg Gly	cag Gln	ttg Leu	cat His 405	cca Pro	cgt Arg	aca Thr	cag Gln	1252
Gly 410	Val	Glu	Thr	Leu	Gly 415	acg Thr	Ile	Tyr	Ser	Ser 420	Ser	Leu	Phe	Pro	Asn 425	1300
Arg	Ala	Pro	Lys	Gly 430	Arg	gtg Val	Leu	Leu	Leu 435	Asn	Tyr	Ile	Gly	Gly 440	Ala	1348
Lys	Asn	Pro	Glu 445	Ile	Leu	tct Ser	Lys	Thr 450	Glu	Ser	Gln	Leu	Val 455	Glu	Val	1396
gtt Val	Asp	Arg 460	Asp	Leu	Arg	Lys	Met 465	Leu	Ile	Lys	Pro	Lys 470	Ala	Gln	Asp	1444
	Leu 475	Val	Val	Gly	Val	Arg 480	Val	Trp	Pro	Gln	Ala 485	Ile	Pro	Gln	Phe	1492
ttg (gtt (Val (ggt Gly	cat His	ctg Leu	gat Asp	acg (cta Leu	agt Ser	act Thr	gca Ala	aaa Lys	gct Ala	gct Ala	atg Met	aat Asn	1540

490	4	195	500		505
gat aa Asp As	t ggg ctt gaa g n Gly Leu Glu G 510	ggg ctg ttt ctt Gly Leu Phe Leu	ggg ggt Gly Gly 515	aat tat gtg Asn Tyr Val	tca ggt 1588 Ser Gly 520
gta go Val Al	a ttg ggg agg t a Leu Gly Arg C 525	gt gtt gaa ggt Cys Val Glu Gly 530	gct tat Ala Tyr	gaa gtt gca Glu Val Ala 535	tcc gag 1636 Ser Glu
	a gga ttt ctg t r Gly Phe Leu S 540			tga aacctgto	gtt 1682
gggggt	agtc caaaccttgt	tagtagtacg at	catgcctt	gggaaaattg g	gcatgtgcct 1742
aaaagt	tttg ctcattagag	g ttattttagc ct	tggtaaat	gatttgtact t	gatatcagt 1802
cgtttt	cttt gagataaaat	gtteetgtte ag	gaaatata	atgtatatca a	attttaaaca 1862
aaaaaa	aaaa aa				1874
<210> <211> <212> <213> <220> <223> <400> attggt <211> <211> <212> <213>	artificial seq lambda-gt22A f 4 ggcg acgactcctg 5 24 DNA	orward primer			23
<220> <223>	lambda-gt22A r	everse primer			
<400> ccagac	5 caac tggtaatggt	agcg			24
<210><211><211><212><213>	24 DNA	quence			
<223>	forward primer	-			

<400>		~ .
gcggtct	taca agtcaggcag tcat	24
<210>	7	
<211>	31	
	DNA	
<213>	artificial sequence	
<220>		
	reverse primer	
<4437	reverse brimer	
<400>	7	
catqcca	aatt ttcccaaggc atgatcgtac t	31
<210>	8	
<211>	20	
<212>	DNA	
	artificial sequence	
(21)/	artificial bequence	
<220>		
<223>	mutagenic primer	
<400>	8	
		20
ggtgtti	tatg ttggtgatcc	20
<210>	9	
<211>		
<212>		
<213>	artificial sequence	
<220>		
	gray and manufactured mainer	
<223>	CaMV 35S promoter forward primer	
<400>	9	
cacagat	tggt tagagaggct tacgcac	27
ouougu.		
<210>	10	
<211>	27	
<212>	DNA	
<213>	artificial sequence	
<220>		
<223>	Nos terminator reverse primer	
	-	
400	10	
<400>	10	27
tcatcg	caag accggcaaca ggattca	27
<210>	11	
<211>	537	
<212>	PRT	

<213> Arabidopsis thaliana

<400> 11

Met Glu Leu Ser Leu Leu Arg Pro Thr Thr Gln Ser Leu Leu Pro Ser 1 10 15

Phe Ser Lys Pro Asn Leu Arg Leu Asn Val Tyr Lys Pro Leu Arg Leu 20 25 30

Arg Cys Ser Val Ala Gly Gly Pro Thr Val Gly Ser Ser Lys Ile Glu 35 40 45

Gly Gly Gly Gly Thr Thr Ile Thr Thr Asp Cys Val Ile Val Gly Gly 50 55 60

Gly Ile Ser Gly Leu Cys Ile Ala Gln Ala Leu Ala Thr Lys His Pro 65 70 75 80

Asp Ala Ala Pro Asn Leu Ile Val Thr Glu Ala Lys Asp Arg Val Gly 85 90 95

Gly Asn Ile Ile Thr Arg Glu Glu Asn Gly Phe Leu Trp Glu Glu Gly
100 105 110

Pro Asn Ser Phe Gln Pro Ser Asp Pro Met Leu Thr Met Val Val Asp 115 120 125

Ser Gly Leu Lys Asp Asp Leu Val Leu Gly Asp Pro Thr Ala Pro Arg 130 135 140

Phe Val Leu Trp Asn Gly Lys Leu Arg Pro Val Pro Ser Lys Leu Thr 145 150 155 160

Asp Leu Pro Phe Phe Asp Leu Met Ser Ile Gly Gly Lys Ile Arg Ala 165 170 175

Gly Phe Gly Ala Leu Gly Ile Arg Pro Ser Pro Pro Gly Arg Glu Glu 180 185 190

Ser Val Glu Glu Phe Val Arg Arg Asn Leu Gly Asp Glu Val Phe Glu 195 200 205

Arg Leu Ile Glu Pro Phe Cys Ser Gly Val Tyr Ala Gly Asp Pro Ser 210 215 220

Lys Leu Ser Met Lys Ala Ala Phe Gly Lys Val Trp Lys Leu Glu Gln 225 230 235 240

Asn Gly Gly Ser Ile Ile Gly Gly Thr Phe Lys Ala Ile Gln Glu Arg 245 250 255

Lys Asn Ala Pro Lys Ala Glu Arg Asp Pro Arg Leu Pro Lys Pro Gln 260 265 270

- Gly Gln Thr Val Gly Ser Phe Arg Lys Gly Leu Arg Met Leu Pro Glu 275 280 285
- Ala Ile Ser Ala Arg Leu Gly Ser Lys Val Lys Leu Ser Trp Lys Leu 290 295 300
- Ser Gly Ile Thr Lys Leu Glu Ser Gly Gly Tyr Asn Leu Thr Tyr Glu 305 310 315 320
- Thr Pro Asp Gly Leu Val Ser Val Gln Ser Lys Ser Val Val Met Thr 325 330 335
- Val Pro Ser His Val Ala Ser Gly Leu Leu Arg Pro Leu Ser Glu Ser 340 345 350
- Ala Ala Asn Ala Leu Ser Lys Leu Tyr Tyr Pro Pro Val Ala Ala Val 355 360 365
- Ser Ile Ser Tyr Pro Lys Glu Ala Ile Arg Thr Glu Cys Leu Ile Asp 370 375 380
- Gly Glu Leu Lys Gly Phe Gly Gln Leu His Pro Arg Thr Gln Gly Val 385 390 395 400
- Glu Thr Leu Gly Thr Ile Tyr Ser Ser Ser Leu Phe Pro Asn Arg Ala 405 410 415
- Pro Pro Gly Arg Ile Leu Leu Leu Asn Tyr Ile Gly Gly Ser Thr Asn 420 425 430
- Thr Gly Ile Leu Ser Lys Ser Glu Gly Glu Leu Val Glu Ala Val Asp 435 440 445
- Arg Asp Leu Arg Lys Met Leu Ile Lys Pro Asn Ser Thr Asp Pro Leu 450 460
- Lys Leu Gly Val Arg Val Trp Pro Gln Ala Ile Pro Gln Phe Leu Val 465 470 475 480
- Gly His Phe Asp Ile Leu Asp Thr Ala Lys Ser Ser Leu Thr Ser Ser 485 490 495
- Gly Tyr Glu Gly Leu Phe Leu Gly Gly Asn Tyr Val Ala Gly Val Ala
 500 505 510
- Leu Gly Arg Cys Val Glu Gly Ala Tyr Glu Thr Ala Ile Glu Val Asn 515 520 525
- Asn Phe Met Ser Arg Tyr Ala Tyr Lys 530 535